

Cytological and Transcriptomic Analyses of Petaloid-type Cytoplasmic Male Sterility in *Camellia oleifera*

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Camellia oleifera is one of the most important woody edible oil seed crop species in China. Although sterile male *C. oleifera* plants play an important role in hybrid breeding, the possible genetic basis of pollen abortion still unclear. In this study, a genic petaloid-type sterile male *C. oleifera* ‘HSP’ plant was investigated using a cytological method and transcriptome analysis. The results showed that in male-fertile plants, anther development was divided into eight stages. But in male sterile plants, pollen abortion occurred from the microspore stage to the mature pollen period. Following transcriptome sequencing, 46,612 unigenes were identified in *C. oleifera*. Functional analysis showed that most of the differentially expressed gene expression were involved in the phenylpropanoid biosynthesis and phytohormone signal transduction pathways. Moreover, weighted gene co-expression network analysis (WGCNA) revealed that 8 candidate genes were likely involved in the formation and development of petaloid stamens, including *CoCPI*, *CoCP2*, *CoAP2*, *CoGH3*, *CoARR-A*, *CoPHEN1* and *CoIAA1*. we propose a hypothetical model of gene expression network that regulates the development of petaloid stamens. This findings provide valuable insight into the complex molecular mechanism of male sterility in *C. oleifera* and also lay a solid foundation for oil tea hybrid breeding.